## Amendments to Specification

Please replace the following paragraphs:

**Paragraph beginning on page 39, line 15**

Amplification was carried out in two steps. The first amplification reaction was performed using 1 μL of first strand cDNA and primer set one (SEQ ID NO:11 and SEQ ID NO:12) with 30 cycles of 94°C for 30 seconds, 50°C for 30 seconds and 72°C for one minute. A second amplification reaction was done with 1 μL of the resulting product with primer set two (SEQ ID NO:13 and SEQ ID NO:14) and using 30 cycles of 94°C for 30 seconds, 50.5°C for 30 seconds and 72°C for one minute. The resulting PCR sequence was cloned into pCR2.1 using TOPO™ TA Cloning Kit (Invitrogen). Plasmid DNA was purified using QIAFilter cartridges (Qiagen Inc) or Wizard Plus Minipreps DNA Purification System (Promega) following the manufacturer's instructions. Sequence was generated on an ABI Automatic sequencer using dye terminator technology and using a combination of vector and insert-specific primers. Sequence editing was performed using DNAStar (DNASTAR, Inc.). All sequences represent coverage at least two times in both directions. The nucleotide sequence comprising the cDNA insert in clone sugarbeet 1 is shown in SEQ ID NO:47; the deduced amino acid sequence of this DNA is shown in SEQ ID NO:48. The nucleotide sequence comprising the cDNA insert in clone sugarbeet 2 is shown in SEQ ID NO:60[[61]]; the deduced amino acid sequence of this DNA is shown in SEQ ID NO:61.

**Paragraph beginning on page 41, line 13:**

A consensus sequence was determined by aligning the amino acid sequences of the present invention using the Clustal method of alignment and this sequence is shown in SEQ ID NO:66. Amino acids not conserved are indicated by Xaa. These are:

| | |
|---|---|
| $Xaa_{10}$ | Phe or Leu |
| $Xaa_{16}$ | Ser or Leu |
| $Xaa_{23}$ | Ser or Thr |
| $Xaa_{25}$ | Ile or Lys |
| $Xaa_{39}$ | Lys or Arg |
| $Xaa_{48}$ | Pro or Leu |
| $Xaa_{60}$ | Pro or Leu |
| $Xaa_{73}$ | Leu or His |
| $Xaa_{74}$ | Ser or Tyr |
| $Xaa_{95}$ | Ala or Thr |

$Xaa_{96}$ Asn or His
$Xaa_{102}$ Asn or Ser
$Xaa_{110}$ Ile, Val, or Thr
$Xaa_{112}$ Arg or His
$Xaa_{117}$ Asn or Ser
$Xaa_{118}$ Ser or Leu
$Xaa_{121}$ Met or Arg
$Xaa_{122}$ Ala or Val
$Xaa_{124}$ Phe or Ile
$Xaa_{129}$ Lys or Arg
$Xaa_{147}$ Lys or Glu
$Xaa_{159}$ Leu or Phe
$Xaa_{162}$ Ala or Val
$Xaa_{166}$ Ser or Gly
$Xaa_{170}$ Gln or Arg
$Xaa_{175}$ Val or Leu
$Xaa_{183}$ Ala or Thr
$Xaa_{187}$ Thr or Ile
$Xaa_{191}$ Met or Val
$Xaa_{209}$ Phe or Tyr
$Xaa_{219}$ Arg or Trp
$Xaa_{223}$ Tyr or His
$Xaa_{253}$ Gly or Glu
$Xaa_{259}$ Lys or Glu
$Xaa_{263}$ Val or Asp
$Xaa_{264}$ Val, Asp, or Ile
$Xaa_{268}$ Ala or Val
$Xaa_{272}$ Phe or Leu
$Xaa_{285}$ Thr or Met
~~$Xaa_{293}$ Glu or Asp~~
$\underline{Xaa_{292}}$ $\underline{Glu\ or\ Asp}$
$\underline{Xaa_{293}}$ $\underline{Gln\ or\ His}$
$\underline{Xaa_{294}}$ $\underline{Thr\ or\ Ile}$
~~$Xaa_{294}$ Thr, or Ile~~
$Xaa_{301}$ Phe or Leu
$Xaa_{306}$ Thr or Ile
$Xaa_{311}$ Val or Glu
$Xaa_{312}$ Val or Ala

| | |
|---|---|
| $Xaa_{325}$ | Arg or Lys |
| $Xaa_{328}$ | Gln or Glu |
| $Xaa_{329}$ | Lys or Arg |
| $Xaa_{334}$ | Val or Ala |
| $Xaa_{342}$ | Arg or Ile |
| $Xaa_{377}$ | Thr or Ile |
| $Xaa_{381}$ | Glu or Gly |
| $Xaa_{385}$ | Tyr, His, or Cys |
| $Xaa_{387}$ | Ile or Thr |
| $Xaa_{393}$ | Val or Ile |
| $Xaa_{394}$ | Leu or Pro |
| $Xaa_{402}$ | Arg or Lys |
| $Xaa_{404}$ | Ser or Pro |
| $Xaa_{413}$ | Ser or Phe |
| $Xaa_{422}$ | Glu or Gly |
| $Xaa_{428}$ | Gly or Arg |
| $Xaa_{429}$ | Pro or Leu |
| $Xaa_{435}$ | Gln or Arg |
| $Xaa_{447}$ | Arg or Gly |
| $Xaa_{453}$ | Asn, Ser, or Ile |
| $Xaa_{459}$ | Met or Thr, and |
| $Xaa_{485}$ | Asp or Gly |

**Please replace the sequence listing** with the enclosed amended sequence listing.